We claim:

1. A peptide fragment having the general sequence

$His-X^1-His-X^2-X^3-X^4-Cys-X^5-X^6-Cys$,

where the variables X^1 to X^6 in the sequence have the following meanings:

X^1 = an amino acid selected from the group of Ala, Val, Phe, Ser, Met, Trp, Tyr, Asn, Asp or Lys and the variables X^2 to X^6 an amino acid selected from the group of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

X^2 = an amino acid selected from the group of Val, Ile, Phe, Pro, Trp, Tyr, Gln, Glu or Arg and the variables X^1, X^3 to X^6 an amino acid selected from the group of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

X^3 = an amino acid selected from the group of Gly, Ile, Thr, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His and the variables X^1, X^2, X^4 to X^6 an amino acid selected from the group of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

X^4 = an amino acid selected from the group of Val, Phe, Pro, Cys, Met, Trp, Asn, Glu, Arg or His and the variables X^1 to X^3, X^5, X^6 an amino acid selected from the group of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

X^5 = an amino acid selected from the group of Gly, Ser, Cys, Met, Trp, Asn, Glu, Lys or Arg and the variables X^1 to X^4, X^6 an amino acid selected from the group of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

X^6 = an amino acid selected from the group of Phe, Pro, Ser, Cys, Trp, Tyr or Gln and the variables X^1 to X^5 an amino acid selected from the group of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His and

where at least one of the variables X^1 to X^6 in the sequence is, independently of one another, Gln or Asn.

2. A peptide fragment as claimed in claim 1, in which the variables X^1 to X^6 have the meanings stated in claim 1, where at least one of the variables X^1 to X^6 in the sequence is, independently of one another, Lys or Arg.

3. A peptide fragment as claimed in claim 1 ~~or 2~~, in which the variables X^1 to X^6 in the sequence have the following meanings independently of one another:

X^1 = an amino acid selected from the group of Ala, Val, Phe, Ser, Met, Trp, Tyr, Asn, Asp or Lys;

X^2 = an amino acid selected from the group of Val, Ile, Phe, Pro, Trp, Tyr, Gln, Glu or Arg;

X^3 = an amino acid selected from the group of Gly, Ile, Thr, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg or His;

X^4 = an amino acid selected from the group of Val, Phe, Pro, Cys, Met, Trp, Asn, Glu, Arg or His;

X^5 = an amino acid selected from the group of Gly, Ser, Cys, Met, Trp, Asn, Glu, Lys or Arg;

X^6 = an amino acid selected from the group of Phe, Pro, Ser, Cys, Trp, Tyr or Gln.

4. A peptide fragment as claimed in ~~any of claims 1 to 3~~ claim 1, in which the variables X^1 to X^6 in the sequence have the following meanings independently of one another:

X^1 = an amino acid selected from the group of Phe, Ser, Asn, Asp or Lys;

X^2 = an amino acid selected from the group of Val, Ile, Phe, Pro, Gln, Glu or Arg;

X^3 = an amino acid selected from the group of Gly, Ile, Thr, Met, Trp, Tyr, Asn, Asp, Glu, Arg or His;

X^4 = an amino acid selected from the group of Val, Phe, Cys, Met, Trp, Asn, Arg or His;

X^5 = an amino acid selected from the group of Gly, Ser, Cys, Met, Asn, Glu, Lys or Arg;

X^6 = an amino acid selected from the group of Phe, Ser, Cys, or Tyr.

5. A peptide fragment as claimed in ~~any of claims 1 to 4~~ claim 1, in which the variables X^1 to X^6 in the sequence have the following meanings independently of one another:

X^1 = Asn;

X^2 = Gln, Glu or Arg;

X^3 = Gly, Thr or Tyr;

X^4 = Asn or Arg;

X^5 = Gly or Lys;

X^6 = Cys.

6. A peptide fragment having the sequence

His-Gln-His-Glu-Gly-Arg-Cys-Lys-Glu-Cys

His-Asn-His-Arg-Tyr-Gly-Cys-Gly-Cys-Cys

His-Arg-His-Gly-Thr-Asn-Cys-Leu-Lys-Cys

His-Ile-His-Gln-Ser-Asn-Cys-Gln-Val-Cys.

7. A fusion protein comprising a protein fragment as claimed in ~~any of claims 1 to 6~~. claim 1

8. A nucleic acid fragment coding for a protein fragment as claimed in ~~any of claims 1 to 6~~. claim 1

9. A nucleic acid comprising a nucleic acid fragment as claimed in claim 8.

10. A nucleic acid coding for a fusion protein as claimed in claim 7.

11. A vector comprising a nucleic acid fragment as claimed in claim 8 ~~or 10~~.

12. A process for preparing fusion proteins as claimed in claim 7, which comprises fusing a nucleic acid fragment ~~as claimed in claim 8~~ to a gene which codes for a protein.

13. A process for purifying fusion proteins as claimed in claim 7, which comprises

a) bringing liquids which contain the fusion protein into contact with immobilized metal ions in such a way that an affinity linkage can form between the metal ions and the fusion protein,

b) removing unbound substances present in the liquid,

c) eluting the bound fusion protein by abolishing the affinity linkage by changing the liquid medium and

d) collecting the purified fusion protein.

14. The use of a protein fragment as claimed in ~~any of claims 1 to 6 or~~ Claim 1 of a nucleic acid fragment ~~as claimed in claim 8~~ for purifying proteins.

15. A process for preparing protein fragments able to enter into a reversible affinity linkage with immobilized metal ions, which comprises carrying out the following steps:

a) preparing a nucleic acid library starting from any suitable nucleic acid sequence which codes for a protein fragment of the sequence

$His\text{-}X^1\text{-}His\text{-}X^2\text{-}X^3\text{-}X^4\text{-}Cys\text{-}X^5\text{-}X^6\text{-}Cys$,

where the histidine and cysteine residues of the sequence are conserved in the nucleic acid library,

b) fusing the nucleic acids of the library to a reporter gene which makes it possible to detect the fusion protein encoded by the resulting nucleic acid via its binding to the immobilized metal ions and

c) selecting the nucleic acid sequences which display a reversible binding to the immobilized metal ions which is at least 1.5 times stronger than the sequence in the natural Helicobacter pylori ATPase-439.

16. A process as claimed in claim 15, wherein the egf protein from Aequoria victoria is used as reporter gene.

17. A method for detecting proteins, which comprises detecting individual proteins which comprise a protein fragment as claimed in claim 1 in a protein mixture via antibodies which are directed against the protein fragment.

18. The use of a protein fragment as claimed in ~~any of claims 1 to 6 or~~ claim 1 of a nucleic acid fragment ~~as claimed in claim 8~~ for purifying proteins.